

**Additional File 1.** Gene loci identified as being under intragenic homologous recombination using the 4 methods of Substitution analysis of recombination (p-value < 0.05).

GENECONV			
Gene locus Tag	locus	Annotation	p-value
CT643	<i>topA</i>	DNA topoisomerase I/SWI domain fusion protein	0
CT852	<i>yhgN</i>	YhgN family protein/putative integral membrane protein	0
CT652	<i>recD_2</i>	exodeoxyribonuclease V alpha chain	0
CT869	<i>pmpE</i>	polymorphic outer membrane protein	0
CT870	<i>pmpF</i>	polymorphic outer membrane protein	0
CT872	<i>pmpH</i>	polymorphic outer membrane protein	0
CT011	-	hypothetical protein	0
CT049	-	hypothetical protein	0
CT144	-	hypothetical protein	0
CT244	-	hypothetical protein	0
CT674	<i>yscC</i>	Yop proteins translocation protein C/general secretion pathway protein/Type III secretion structural protein (outer membrane ring)	0
CT678	<i>pyrH</i>	uridylate kinase	0
CT679	<i>tsf</i>	elongation factor Ts	0
CT681	<i>ompA</i>	major outer membrane protein	0
CT682	<i>pbpB</i>	penicillin-binding protein	0
CT402	<i>lpxK</i>	tetraacyldisaccharide 4'-kinase	0
CT448	<i>secD/secF</i>	bifunctional preprotein translocase subunit SecD/SecF	0
CT604	<i>GroEL_2</i>	HSP-60/60 kDa chaperonin GroEL2	0
CT619	-	hypothetical protein	0
CT107	<i>mutY</i>	A/G-specific adenine glycosylase	0.0003
CT456	-	Hypothetical protein/Translocated actin-recruiting phosphoprotein (tarp protein)	0.0004
CT675	<i>karG</i>	ATP:guanido phosphotransferase	0.0011
CT676	-	hypothetical protein	0.0015
CT653	<i>yhbG</i>	ABC transporter ATP-binding protein	0.0046
CT112	<i>pepF</i>	oligoendopeptidase F	0.0127
CT685	-	ABC transporter ATP-binding protein	0.0135
CT052	<i>hemN_1</i>	coproporphyrinogen III oxidase	0.0332
CT873	-	hypothetical protein	0.0425
<b>Maximum <math>\chi^2</math></b>			
Gene	locus	Annotation	p-value

locus Tag			
CT674	<i>yscC</i>	Type III secretion structural protein (outer membrane ring)	0.00E+00
CT681	<i>ompA</i>	major outer membrane protein	0.00E+00
CT869	<i>pmpE</i>	polymorphic outer membrane protein	0.00E+00
CT870	<i>pmpF</i>	polymorphic outer membrane protein	0.00E+00
CT872	<i>pmpH</i>	polymorphic outer membrane protein	0.00E+00
CT049	-	hypothetical protein	0.00E+00
CT144	-	hypothetical protein	0.00E+00
CT456	-	Translocated actin-recruiting phosphoprotein (tarp protein)	0.00E+00
CT619	-	hypothetical protein	0.00E+00
CT679	<i>tsf</i>	elongation factor Ts	0.00E+00
CT871	<i>pmpG</i>	polymorphic outer membrane protein	0.00E+00
CT640	<i>recC</i>	exodeoxyribonuclease V gamma chain	0.00E+00
CT682	<i>pbpB</i>	penicillin-binding protein	0.00E+00
CT448	<i>secD/se cF</i>	bifunctional preprotein translocase subunit SecD/SecF	0.00E+00
CT011	-	hypothetical protein	0.00E+00
CT244	-	hypothetical protein	0.00E+00
CT402	<i>lpxK</i>	tetraacyldisaccharide 4'-kinase	0.00E+00
CT604	<i>GroEL_2</i>	60 kDa chaperonin GroEL2	0.00E+00
CT680	<i>rpsB</i>	30S ribosomal protein S2	1.00E-03
CT653	<i>yhbG</i>	ABC transporter ATP-binding protein	1.00E-03
CT852	<i>yhgN</i>	YhgN family protein/putative integral membrane protein	1.00E-03
CT675	<i>karG</i>	ATP:guanido phosphotransferase	2.00E-03
CT652	<i>recD_2</i>	exodeoxyribonuclease V alpha chain	2.00E-03
CT684	-	cysteine desulfurase activator complex subunit SufB	2.00E-03
CT678	<i>pyrH</i>	uridylate kinase	3.00E-03
CT676	-	hypothetical protein	4.00E-03
CT470	<i>recO</i>	DNA repair protein RecO	4.00E-03
CT621	-	hypothetical protein	4.00E-03
CT875	-	hypothetical protein	8.00E-03
CT677	<i>frr</i>	ribosome recycling factor	8.00E-03
CT295	<i>mrsA_1</i>	phosphoglucomutase	8.00E-03
CT686	-	hypothetical protein	9.00E-03
CT115	-	inclusion membrane protein D	1.10E-02
CT580	-	Hypothetical protein/putative integral membrane protein	1.10E-02
CT642	-	hypothetical protein	1.20E-02
CT685	-	ABC transporter ATP-binding protein	1.30E-02

CT683	-	TPR-motif-containing protein/tetratricopeptide repeat protein	1.30E-02
CT688	<i>parB</i>	putative chromosome partitioning protein	1.40E-02
CT107	<i>mutY</i>	A/G-specific adenine DNA glycosylase	1.90E-02
CT727	<i>zntA</i>	metal transport P-type ATPase/cation transporting ATPase	1.90E-02
CT551	<i>dacC</i>	D-alanyl-D-alanine carboxypeptidase	2.00E-02
CT315	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta	2.10E-02
CT650	<i>recA</i>	recombinase A	2.20E-02
CT145	-	serine/threonine-protein kinase PKN1	2.70E-02
CT643	<i>topA</i>	DNA topoisomerase I/SWI domain fusion protein	3.00E-02
CT020	<i>lepB</i>	signal peptidase I	4.00E-02
CT874	<i>pmpI</i>	polymorphic outer membrane protein	4.60E-02

#### Pairwise Homoplasy Index (PHI)

Gene locus Tag	locus	Annotation	p-value
CT680	<i>rpsB</i>	30S ribosomal protein S2	0.00E+00
CT681	<i>ompA</i>	major outer membrane protein	0.00E+00
CT869	<i>pmpE</i>	polymorphic outer membrane protein	0.00E+00
CT870	<i>pmpF</i>	polymorphic outer membrane protein	0.00E+00
CT872	<i>pmpH</i>	polymorphic outer membrane protein	0.00E+00
CT049	-	hypothetical protein	0.00E+00
CT144	-	hypothetical protein	0.00E+00
CT679	<i>tsf</i>	elongation factor Ts	1.00E-02
CT824	-	insulinase family metalloprotease	1.70E-02
CT676	-	hypothetical protein	2.90E-02
CT677	<i>frr</i>	ribosome recycling factor	3.40E-02
CT674	<i>yscC</i>	Type III secretion structural protein	4.30E-02
CT686	-	ABC transporter membrane protein	4.80E-02

#### Neighbor Similarity Score (NSS)

Gene locus Tag	locus	Annotation	p-value
CT674	<i>yscC</i>	Type III secretion structural protein	0.00E+00
CT675	<i>karG</i>	ATP:guanido phosphotransferase	0.00E+00
CT680	<i>rpsB</i>	30S ribosomal protein S2	0.00E+00

CT681	<i>ompA</i>	major outer membrane protein	0.00E+00
CT686	-	ABC transporter membrane protein	0.00E+00
CT869	<i>pmpE</i>	polymorphic outer membrane protein	0.00E+00
CT870	<i>pmpF</i>	polymorphic outer membrane protein	0.00E+00
CT872	<i>pmpH</i>	polymorphic outer membrane protein	0.00E+00
CT049	-	hypothetical protein	0.00E+00
CT144	-	hypothetical protein	0.00E+00
CT824	-	metalloprotease-insulinase	5.00E-03
CT288	-	Hypothetical protein/candidate inclusion membrane protein	5.00E-03
CT838	-	hypothetical protein/putative membrane transport protein	6.00E-03
CT456	-	Translocated actin-recruiting phosphoprotein (Tarp)	7.00E-03
CT619	-	hypothetical protein	7.00E-03
CT700	-	hypothetical protein	9.00E-03
CT679	<i>tsf</i>	elongation factor Ts	1.60E-02
CT871	<i>pmpG</i>	polymorphic outer membrane protein	1.70E-02
CT640	<i>recC</i>	exodeoxyribonuclease V gamma chain	3.20E-02
CT682	<i>pbpB</i>	penicillin-binding protein	4.40E-02
CT033	<i>recD_I</i>	exodeoxyribonuclease V alpha chain	4.40E-02